#2

OIPE

RAW SEQUENCE LISTING   DATE: 07/07/2001
PATENT APPLICATION: US/09/891,609   TIME: 14:37:46

Input Set : **A:\2570-1-002N sequence listing.ST25.txt**
Output Set: **N:\CRF3\07062001\I891609.raw**

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 3 <110> APPLICANT: Stamatatos, Leondias
 5 <120> TITLE OF INVENTION: HIV-1 VACCINES AND SCREENING METHODS THEREFOR
 7 <130> FILE REFERENCE: 2570-1-002N
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C--> ` 9 <140> CURRENT APPLICATION NUMBER: US/09/891,609`
C--> ` 9 <141> CURRENT FILING DATE: 2001-06-26`
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 9 <150> PRIOR APPLICATION NUMBER: 60/214,608
10 <151> PRIOR FILING DATE: 2000-06-27
12 <160> NUMBER OF SEQ ID NOS: 4
14 <170> SOFTWARE: PatentIn version 3.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 1941
18 <212> TYPE: DNA
19 <213> ORGANISM: Human immunodeficiency virus type 1
21 <400> SEQUENCE: 1
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ENTERED

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24 cttgggatgt tgatgatctg tagtgctgta gaaaaattgt gggtcacagt ctattatggg   120
26 gtacctgtgt ggaaagaagc aaccaccact ctattttgtg catcagatgc taaagcctat   180
28 gacacagagg tacataatgt ctgggccaca catgcctgtg tacccacaga ccctaaccca   240
30 caagaaatag tattggaaaa tgtgacagaa aattttaaca tgtggaaaaa taacatggta   300
32 gaacagatgc atgaggatat aatcagttta tgggatcaaa gtctaaagcc atgtgtaaag   360
34 ttaaccccac tctgtgttac tctacattgc actaatttga agaatgctac taataccaag   420
36 agtagtaatt ggaaagagat ggacagagga gaaataaaaa attgctcttt caaggtcgga   480
38 gctggaaaat tgataaattg taacacctca gtcattacac aggcctgtcc aaaggtatcc   540
40 tttgaaccaa ttcccataca ttattgtgcc ccggctggtt ttgcgattct aaagtgtaat   600
42 gataagaagt tcaatggatc aggaccatgt acaaatgtca gcacagtaca atgtacacat   660
44 ggaattaggc cagtagtgtc aactcaattg ctgttaaatg gcagtctagc agaagaaggg   720
46 gtagtaatta gatctgaaaa tttcacagac aatgctaaaa ctataatagt acagctgaag   780
48 gaatctgtag aaattaattg tacaagacct aacaataata caagaaaaag tataactata   840
50 ggaccgggga gagcatttta tgcaacagga gacataatag gagatataag acaagcacat   900
52 tgtaacatta gtggagaaaa atggaataac actttaaaac agatagttac aaaattacaa   960
54 gcacaatttg ggaataaaac aatagtcttt aagcaatcct caggagggga cccagaaatt  1020
56 gtaatgcaca gttttaattg tggaggggaa tttttctact gtaattcaac acagcttttt  1080
58 aatagtactt ggaataatac tataggccca ataacacta atggaactat cacactccca  1140
60 tgcagaataa aacaaattat aaacaggtgg caggaagtag aaaagcaat gtatgccct  1200
62 cccatcagag acaaattag atgctcatca aatattacag gactgctatt aacaagagat  1260
64 ggtggtaaag agatcagtaa caccaccgag atcttcagac ctggaggtgg agatatgagg  1320
66 gacaattgga gaagtgaatt atataaatat aaagtagtaa aaattgagcc attaggagta  1380
68 gcacccacca aggcaaagag aagagtggtg cagagagaaa aaagagcagt gacgctagga  1440
70 gctatgttcc ttgggttctt gggagcagca ggaagcacta tgggcgcacg tcactgacg  1500
72 ctgacggtac aggccagaca attattgtct ggtatagtgc aacagcagaa caatttgctg  1560
74 agagctattg aggcgcaaca gcatctgttg caactcacag tctgggcat caagcagctc  1620
76 caggcaagag tcctggctgt ggaaagatac ctaaaggatc aacagctcct agggatttgg  1680
78 ggttgctctg gaaaactcat ttgcaccact gctgtgcctt ggaatgctag ttggagtaat  1740
80 aaatctctgg atcagatttg gaataacatg acctggatgg agtgggagag agaaattgac  1800
82 aattacacaa acttaatata caccttaatt gaagaatcgc agaaccaaca gaaaagaat  1860
84 gaacaagaat tattagaatt ggataagtgg gcaagtttgt ggaattggtt tgacatatca  1920
86 aaatggctgt ggtatataaa a                                            1941
```

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Input Set : A:\2570-1-002N sequence listing.ST25.txt
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89  <210> SEQ ID NO: 2
90  <211> LENGTH: 646
91  <212> TYPE: PRT
92  <213> ORGANISM: Human immunodeficiency virus type 1
94  <400> SEQUENCE: 2
96  Met Arg Val Lys Gly Ile Arg Lys Asn Tyr Gln His Leu Trp Arg Gly
97  1               5                   10                  15
100 Gly Thr Leu Leu Leu Gly Met Leu Met Ile Cys Ser Ala Val Glu Lys
101             20                  25                  30
104 Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr
105             35                  40                  45
108 Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val
109     50                  55                  60
112 His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
113 65                  70                  75                  80
116 Gln Glu Ile Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys
117             85                  90                  95
120 Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
121             100                 105                 110
124 Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
125             115                 120                 125
128 His Cys Thr Asn Leu Lys Asn Ala Thr Asn Thr Lys Ser Ser Asn Trp
129     130                 135                 140
132 Lys Glu Met Asp Arg Gly Glu Ile Lys Asn Cys Ser Phe Lys Val Gly
133 145                 150                 155                 160
136 Ala Gly Lys Leu Ile Asn Cys Asn Thr Ser Val Ile Thr Gln Ala Cys
137             165                 170                 175
140 Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala
141             180                 185                 190
144 Gly Phe Ala Ile Leu Lys Cys Asn Asp Lys Lys Phe Asn Gly Ser Gly
145             195                 200                 205
148 Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro
149     210                 215                 220
152 Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Gly
153 225                 230                 235                 240
156 Val Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile
157             245                 250                 255
160 Val Gln Leu Lys Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn
161             260                 265                 270
164 Asn Thr Arg Lys Ser Ile Thr Ile Gly Pro Gly Arg Ala Phe Tyr Ala
165             275                 280                 285
168 Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser
169     290                 295                 300
172 Gly Glu Lys Trp Asn Asn Thr Leu Lys Gln Ile Val Thr Lys Leu Gln
173 305                 310                 315                 320
176 Ala Gln Phe Gly Asn Lys Thr Ile Val Phe Lys Gln Ser Ser Gly Gly
177             325                 330                 335
180 Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe Phe
181             340                 345                 350
```

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```
184 Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Asn Thr Ile
185         355             360             365
188 Gly Pro Asn Asn Thr Asn Gly Thr Ile Thr Leu Pro Cys Arg Ile Lys
189     370             375             380
192 Gln Ile Ile Asn Arg Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro
193 385             390             395             400
196 Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu
197             405             410             415
200 Leu Thr Arg Asp Gly Gly Lys Glu Ile Ser Asn Thr Thr Glu Ile Phe
201             420             425             430
204 Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr
205         435             440             445
208 Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys
209     450             455             460
212 Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala Val Thr Leu Gly
213 465             470             475             480
216 Ala Met Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala
217             485             490             495
220 Arg Ser Leu Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile
221         500             505             510
224 Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His
225         515             520             525
228 Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Leu Gln Ala Arg Val Leu
229     530             535             540
232 Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly
233 545             550             555             560
236 Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser
237             565             570             575
240 Trp Ser Asn Lys Ser Leu Asp Gln Ile Trp Asn Asn Met Thr Trp Met
241             580             585             590
244 Glu Trp Glu Arg Glu Ile Asp Asn Tyr Thr Asn Leu Ile Tyr Thr Leu
245         595             600             605
248 Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu
249     610             615             620
252 Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asp Ile Ser Lys
253 625             630             635             640
256 Trp Leu Trp Tyr Ile Lys
257             645
260 <210> SEQ ID NO: 3
261 <211> LENGTH: 1860
262 <212> TYPE: DNA
263 <213> ORGANISM: Human immunodeficiency virus type 1
265 <400> SEQUENCE: 3
266 agtgctgtag aaaaattgtg ggtcacagtc tattatgggg tacctgtgtg gaaagaagca    60
268 accaccactc tattttgtgc atcagatgct aaagcctatg acacagaggt acataatgtc   120
270 tgggccacac atgcctgtgt acccacagac cctaacccac aagaaatagt attggaaaat   180
272 gtgacagaaa attttaacat gtggaaaaat aacatggtag aacagatgca tgaggatata   240
274 atcagtttat gggatcaaag tctaaagcca tgtgtaaagt taaccccact ctgtgttact   300
276 ctacattgca ctaatttgaa gaatgctact aataccaaga gtagtaattg gaaagagatg   360
```

```
278 gacagaggag aaataaaaaa ttgctctttc aaggtcggag ctggaaaatt gataaattgt  420
280 aacacctcag tcattacaca ggcctgtcca aaggtatcct ttgaaccaat tcccatacat  480
282 tattgtgccc cggctggttt tgcgattcta aagtgtaatg ataagaagtt caatggatca  540
284 ggaccatgta caaatgtcag cacagtacaa tgtacacatg gaattaggcc agtagtgtca  600
286 actcaattgc tgttaaatgg cagtctagca gaagaagggg tagtaattag atctgaaaat  660
288 ttcacagaca atgctaaaac tataatagta cagctgaagg aatctgtaga aattaattgt  720
290 acaagaccta acaataatac aagaaaaagt ataactatag gaccggggag agcattttat  780
292 gcaacaggag acataatagg agatataaga caagcacatt gtaacattag tggagaaaaa  840
294 tggaataaca ctttaaaaca gatagttaca aaattacaag cacaatttgg gaataaaaca  900
296 atagtcttta agcaatcctc aggaggggac ccagaaattg taatgcacag ttttaattgt  960
298 ggaggggaat ttttctactg taattcaaca cagctttta atagtacttg gaataatact  1020
300 ataggggccaa ataacactaa tggaactatc acactcccat gcagaataaa acaaattata  1080
302 aacaggtggc aggaagtagg aaaagcaatg tatgcccctc ccatcagagg acaaattaga  1140
304 tgctcatcaa atattacagg actgctatta acaagagatg gtggtaaaga gatcagtaac  1200
306 accaccgaga tcttcagacc tggaggtgga gatatgaggg acaattggag aagtgaatta  1260
308 tataaatata aagtagtaaa aattgagcca ttaggagtag cacccaccaa ggcaaagaga  1320
310 agagtggtgc agagagaaaa aagagcagtg acgctaggag ctatgttcct tgggttcttg  1380
312 ggagcagcag gaagcactat gggcgcacgg tcactgacgc tgacggtaca ggccagacaa  1440
314 ttattgtctg gtatagtgca acagcagaac aatttgctga gagctattga ggcgcaacag  1500
316 catctgttgc aactcacagt ctggggcatc aagcagctcc aggcaagagt cctggctgtg  1560
318 gaaagatacc taaaggatca acagctccta gggatttggg gttgctctgg aaaactcatt  1620
320 tgcaccactg ctgtgccttg gaatgctagt tggagtaata atctctgga tcagatttgg  1680
322 aataacatga cctggatgga gtgggagaga gaaattgaca attacacaaa cttaatatac  1740
324 accttaattg aagaatcgca gaaccaacaa gaaaagaatg aacaagaatt attagaattg  1800
326 gataagtggg caagtttgtg gaattggttt gacatatcaa aatggctgtg gtatataaaa  1860
329 <210> SEQ ID NO: 4
330 <211> LENGTH: 619
331 <212> TYPE: PRT
332 <213> ORGANISM: Human immunodeficiency virus type 1
334 <400> SEQUENCE: 4
336 Ser Ala Val Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val
337 1               5                   10                  15
340 Trp Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala
341             20                  25                  30
344 Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro
345             35                  40                  45
348 Thr Asp Pro Asn Pro Gln Glu Ile Val Leu Glu Asn Val Thr Glu Asn
349         50                  55                  60
352 Phe Asn Met Trp Lys Asn Asn Met Val Glu Gln Met His Glu Asp Ile
353 65                  70                  75                  80
356 Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro
357                 85                  90                  95
360 Leu Cys Val Thr Leu His Cys Thr Asn Leu Lys Asn Ala Thr Asn Thr
361             100                 105                 110
364 Lys Ser Ser Asn Trp Lys Glu Met Asp Arg Gly Glu Ile Lys Asn Cys
365             115                 120                 125
368 Ser Phe Lys Val Gly Ala Gly Lys Leu Ile Asn Cys Asn Thr Ser Val
369         130                 135                 140
372 Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His
```

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373 145                    150                  155                    160
376 Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asp Lys Lys
377             165                 170                 175
380 Phe Asn Gly Ser Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr
381             180                 185                 190
384 His Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser
385             195                 200                 205
388 Leu Ala Glu Glu Gly Val Val Ile Arg Ser Glu Asn Phe Thr Asp Asn
389     210                 215                 220
392 Ala Lys Thr Ile Ile Val Gln Leu Lys Glu Ser Val Glu Ile Asn Cys
393 225                 230                 235                 240
396 Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly Pro Gly
397             245                 250                 255
400 Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala
401             260                 265                 270
404 His Cys Asn Ile Ser Gly Glu Lys Trp Asn Asn Thr Leu Lys Gln Ile
405             275                 280                 285
408 Val Thr Lys Leu Gln Ala Gln Phe Gly Asn Lys Thr Ile Val Phe Lys
409     290                 295                 300
412 Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys
413 305                 310                 315                 320
416 Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr
417             325                 330                 335
420 Trp Asn Asn Thr Ile Gly Pro Asn Asn Thr Asn Gly Thr Ile Thr Leu
421             340                 345                 350
424 Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg Trp Gln Glu Val Gly Lys
425             355                 360                 365
428 Ala Met Tyr Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn
429     370                 375                 380
432 Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Lys Glu Ile Ser Asn
433 385                 390                 395                 400
436 Thr Thr Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp
437             405                 410                 415
440 Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly
441             420                 425                 430
444 Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg
445             435                 440                 445
448 Ala Val Thr Leu Gly Ala Met Phe Leu Gly Phe Leu Gly Ala Ala Gly
449     450                 455                 460
452 Ser Thr Met Gly Ala Arg Ser Leu Thr Leu Thr Val Gln Ala Arg Gln
453 465                 470                 475                 480
456 Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile
457             485                 490                 495
460 Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Leu
461             500                 505                 510
464 Gln Ala Arg Val Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu
465             515                 520                 525
468 Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
469     530                 535                 540
```

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date